(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
15 April 2004 (15.04.2004)

PCT

(10) International Publication Number
WO 2004/030615 A2

(51) International Patent Classification[7]: A61K

(21) International Application Number:
PCT/US2003/028547

(22) International Filing Date:
29 September 2003 (29.09.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/414,971 2 October 2002 (02.10.2002) US

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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 2004/030615 A2

(54) Title: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

(57) Abstract: The present invention is directed to compositions of matter useful for the diagnosis and treatment of tumor in mammals and to methods of using those compositions of matter for the same.

APPENDIX

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RESULT 15
ABM81255
ID   ABM81255 standard; protein; 1019 AA.
XX
AC   ABM81255;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Tumour-associated antigenic target (TAT) polypeptide PRO81993, SEQ:3235.
XX
OS   Homo sapiens.
XX
PN   WO2004030615-A2.
XX
PD   15-APR-2004.
XX
PF   29-SEP-2003; 2003WO-US028547.
XX
PR   02-OCT-2002; 2002US-0414971P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wu TD,  Zhang Z,  Zhou Y;
XX
DR   WPI; 2004-347921/32.
DR   N-PSDB; ACN39223.
XX
PT   New tumor-associated antigenic target polypeptides and nucleic acids,
PT   useful in preparing a medicament for treating or detecting a
PT   proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT   prostate cancer or tumor.
XX
PS   Claim 12; SEQ ID NO 3235; 7273pp; English.
XX
CC   The invention relates to human tumour-associated antigenic target (TAT)
CC   polypeptides, and their related nucleic acids. The TAT polypeptides are
CC   overexpressed in cancer tissues compared to normal tissues, and may thus
CC   serve as effective targets for the diagnosis and treatment of cancer in
CC   mammals. The invention also relates to nucleic acid and polypeptide
CC   sequences at least 80% identical to the TAT nucleic acids and
CC   polypeptides; expression vectors and host cells comprising a TAT nucleic
CC   acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC   molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC   TAT polypeptide; and methods and compositions for the treatment or
CC   diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC   antibodies, antagonists, binding molecules and compositions are useful
CC   for diagnosing or treating a cell proliferative disorder associated with
CC   increased TAT expression, particularly cancers such as breast cancer,
CC   colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC   cancer, pancreatic cancer, cervical cancer, cancers of the central
CC   nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC   used as hybridisation probes, in chromosome and gene mapping, in
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CC   chromosome identification and in gene therapy. The present sequence
CC   represents a TAT polypeptide of the invention
XX
SQ   Sequence 1019 AA;

  Query Match             85.2%;  Score 5152;  DB 8;  Length 1019;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  992;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps
0;

Qy        170 AAQELSQEIKAFLTGVDPILGHQLSAREHARCGLLLLRSLPPARAAVLDHLRGVFDESVR 229
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 SAQELSQEIKAFLTGVDPILGHQLSAREHARCGLLLLRSLPPARAAVLDHLRGVFDESVR 86

Qy        230 AHLAALDETPVAGPPHLRPPPPSHVPAGGPGLEDVVQEVQQVLSEFIRANPKAWAPVISA 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 AHLAALDETPVAGPPHLRPPPPSHVPAGGPGLEDVVQEVQQVLSEFIRANPKAWAPVISA 146

Qy        290 WSIDLMGQLSSTYSGQHQRVPHATGALNELLQLWMGCRATRTLMDIYVQCLSALIGSCPD 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 WSIDLMGQLSSTYSGQHQRVPHATGALNELLQLWMGCRATRTLMDIYVQCLSALIGSCPD 206

Qy        350 ACVDALLDTSVQHSPHFDWVVAHIGSSFPGTIISRVLSCGLKDFCVHGGAGGGAGSSGGS 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 ACVDALLDTSVQHSPHFDWVVAHIGSSFPGTIISRVLSCGLKDFCVHGGAGGGAGSSGGS 266

Qy        410 SSQTPSTDPFPGSPAIPAEKRVPKIASVVGILGHLASRHGDSIRRELLRMFHDSLAGGSG 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 SSQTPSTDPFPGSPAIPAEKRVPKIASVVGILGHLASRHGDSIRRELLRMFHDSLAGGSG 326

Qy        470 GRSGDPSLQATVPFLLQLAVMSPALLGTVSGELVDCLKPPAVLSQLQQHLQGFPREELDN 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 GRSGDPSLQATVPFLLQLAVMSPALLGTVSGELVDCLKPPAVLSQLQQHLQGFPREELDN 386

Qy        530 MLNLAVHLVSQASGAGAYRLLQFLVDTAMPASVITTQGLAVPDTVREACDRLIQLLLLHL 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 MLNLAVHLVSQASGAGAYRLLQFLVDTAMPASVITTQGLAVPDTVREACDRLIQLLLLHL 446

Qy        590 QKLVHHRGGSPGEGVLGPPPPPRLVPFLDALKNHVGELCGETLRLERKRFLWQHQLLGLL 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 QKLVHHRGGSPGEGVLGPPPPPRLVPFLDALKNHVGELCGETLRLERKRFLWQHQLLGLL 506

Qy        650 SVYTRPSCGPEALGHLLSRARSPEELSLATQLYAGLVVSLSGLLPLAFRSCLARVHAGTL 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 SVYTRPSCGPEALGHLLSRARSPEELSLATQLYAGLVVSLSGLLPLAFRSCLARVHAGTL 566

Qy        710 QPPFTARFLRNLALLVGWEQQGGEGPAALGAHFGESASAHLSDLAPLLLHPEEEVAEAAA 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 QPPFTARFLRNLALLVGWEQQGGEGPAALGAHFGESASAHLSDLAPLLLHPEEEVAEAAA 626

Qy        770 SLLAICPFPSEALSPSQLLGLVRAGVHRFFASLRLHGPPGVASACQLLTRLSQTSPAGLK 829
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 SLLAICPFPSEALSPSQLLGLVRAGVHRFFASLRLHGPPGVASACQLLTRLSQTSPAGLK 686
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Qy        830 AVLQLLVEGALHRGNTELFGGQVDGDNETLSVVSASLASASLLDTNRRHTAAVPGPGGIW 889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 AVLQLLVEGALHRGNTELFGGQVDGDNETLSVVSASLASASLLDTNRRHTAAVPGPGGIW 746

Qy        890 SVFHAGVIGRGLKPPKFVQSRNQQEVIYNTQSLLSLLVHCCSAPGGTECGECWGAPILSP 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 SVFHAGVIGRGLKPPKFVQSRNQQEVIYNTQSLLSLLVHCCSAPGGTECGECWGAPILSP 806

Qy        950 EAAKAVAVTLVESVCPDAAGAELAWPPEEHARATVERDLRIGRRFREQPLLFELLKLVAA1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 EAAKAVAVTLVESVCPDAAGAELAWPPEEHARATVERDLRIGRRFREQPLLFELLKLVAA 866

Qy       1010 APPALCYCSVLLRGLLAALLGHWEASRHPDTTHSPWHLEASCTLVAVMAEGSLLPPALGN1069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 APPALCYCSVLLRGLLAALLGHWEASRHPDTTHSPWHLEASCTLVAVMAEGSLLPPALGN 926

Qy       1070 MHEVFSQLAPFEVRLLLLSVWGFLREHGPLPQKFIFQSERGRFIRDFSREGGGEGGPHLA1129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 MHEVFSQLAPFEVRLLLLSVWGFLREHGPLPQKFIFQSERGRFIRDFSREGGGEGGPHLA 986

Qy       1130 VLHSVLHRNIDRLGLFSGRFQAPSPSTLLRQGT 1162
              ||||||||||||||||||||||||||||||||
Db        987 VLHSVLHRNIDRLGLFSGRFQAPSPSTLLRQGT 1019
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3508/6881

FIGURE 3235

MSALCDPPGAPGPPGPAPATHGPAPLSAQELSQEIKAFLTGVDPILGHQLSAREHARCGLLLLRSLPPARAAVLD
HLRGVFDESVRAHLAALDETPVAGPPHLRPPPPSHVPAGGPGLEDVVQEVQQVLSEFIRANPKAWAPVISAWSID
LMGQLSSTYSGQHQRVPHATGALNELLQLWMGCRATRTLMDIYVQCLSALIGSCPDACVDALLDTSVQHSPHFDW
VVAHIGSSFPGTIISRVLSCGLKDFCVHGGAGGGAGSSGGSSSQTPSTDPFPGSPAIPAEKRVPKIASVVGILGH
LASRHGDSIRRELLRMFHDSLAGGSGGRSGDPSLQATVPFLLQLAVMSPALLGTVSGELVDCLKPPAVLSQLQQH
LQGFPREELDNMLNLAVHLVSQASGAGAYRLLQFLVDTAMPASVITTQGLAVPDTVREACDRLIQLLLLHLQKLV
HHRGGSPGEGVLGPPPPPRLVPFLDALKNHVGELCGETLRLERKRFLWQHQLLGLLSVYTRPSCGPEALGHLLSR
ARSPEELSLATQLYAGLVVSLSGLLPLAFRSCLARVHAGTLQPPFTARFLRNLALLVGWEQQGGEGPAALGAHFG
ESASAHLSDLAPLLLHPEEEVAEAAASLLAICPFPSEALSPSQLLGLVRAGVHRFFASLRLHGPPGVASACQLLT
RLSQTSPAGLKAVLQLLVEGALHRGNTELFGGQVDGDNETLSVVSASLASASLLDTNRRHTAAVPGPGGIWSVFH
AGVIGRGLKPPKFVQSRNQQEVIYNTQSLLSLLVHCCSAPGGTECGECWGAPILSPEAAKAVAVTLVESVCPDAA
GAELAWPPEEHARATVERDLRIGRRFREQPLLFELLKLVAAAPPALCYCSVLLRGLLAALLGHWEASRHPDTTHS
PWHLEASCTLVAVMAEGSLLPPALGNMHEVFSQLAPFEVRLLLLSVWGFLREHGPLPQKFIFQSERGRFIRDFSR
EGGGEGGPHLAVLHSVLHRNIDRLGLFSGRFQAPSPSTLLRQGT